

BLAST Basic Local Alignment Search Tool

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Blast 2 sequences

gb|Af011751| (9599 letters)

Results for: gb|AF011751.1 Hepatitis C virus strain H77 pCV-H77C polyprotein gene, complete cds(9599bp)
Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

gi|2327070|gb|AF011751.1|AF011751

Description

Hepatitis C virus strain H77 pCV-H77C polyprotein gene, complete cds

Molecule type

nucleic acid

Query Length

9599

Subject ID

gi|5420376|emb|AJ238799.1|

Description

Hepatitis C virus type 1b complete genome, isolate Con1

Molecule type

nucleic acid

Subject Length

9605

Program

BLASTN 2.2.21+ Citation

Reference

Zheng Zhang, Scott Schwartz, Lukas Wagner, and Webb Miller (2000), "A greedy algorithm for aligning DNA sequences", J Comput Biol 2000; 7(1-2):203-14.

Other reports: [Search Summary](#) [\[Taxonomy reports\]](#)

Search Parameters

Program	blastn
Word size	28
Expect value	10
Hitlist size	100
Match/Mismatch scores	1,-2
Gapcosts	0,0
Low Complexity Filter	Yes
Filter string	L;m;
Genetic Code	1

Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	1.33271	1.28

K	0.620991	0.46
H	1.12409	0.85

Results Statistics

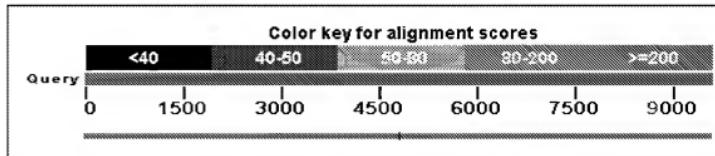
Effective search space 91853047

Graphic Summary

Distribution of 2 Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.



Dot Matrix View

Plot of gi|2327070|gb|AF011751.1|AF011751 vs gi|5420376|emb|AJ238799.1

This dot matrix view shows regions of similarity based upon the BLAST results. The query sequence is represented on the X-axis and the numbers represent the bases/residues of the query. The subject is represented on the Y-axis and again the numbers represent the bases/residues of the subject. Alignments are shown in the plot as lines. Plus strand and protein matches are slanted from the bottom left to the upper right corner, minus strand matches are slanted from the upper left to the lower right. The number of lines shown in the plot is the same as the number of alignments found by BLAST.



Descriptions

Legend for links to other resources: UniGene GEO Gene Structure Map Viewer

Sequences producing significant alignments

(Click headers to sort columns)

AJ238799.1 Hepatitis C virus type 1b complete genome, isolate 5956 9311 99% 0.0 79
Con1

Alignments Select All Get selected sequences Distance tree of results Multiple alignment [NEW](#)>emb|AJ238799.1| Hepatitis C virus type 1b complete genome, isolate Con1
Length=9605Sort alignments for this subject set
E value Score Percent identity
Query start position Subject startScore = 5956 bits (3225), Expect = 0.0
Identities = 7350/9298 (79%), Gaps = 458/9298 (4%)
Strand=Plus/Plus

Query 531	CCTATCCCCAAGGCACGTGCGCCGAGGGCAGGACCTGGCTCAGCCCCGGTACCCCTGG	590
Sbjct 531	CCTATCCCCAAGGCTCGCCAGCCGAGGGTAGGCCCTGGCTCAGCCCCGGTACCCCTGG	590
Query 591	CCCCCTATGGCAATGAGGG-TTGGCGGTGGGGGATGGCTCCTGTCTCCCGTGGCTC	649
Sbjct 591	CCCCCTATGGCAATGAGGGCTTG-GGGTGGCAGGATGGCTCCTGTACCCCGTGGCTC	649
Query 650	TGGCCCTAGCTGGGGCCCCACAGACCCCCCGCGTAGGTCGCAGCAATTGGTAAGGTAT	709
Sbjct 650	TGGCCCTAGTTGGGGCCCCACGGACCCCCCGCGTAGGTCGCAGCAATTGGTAAGGTAT	709
Query 710	CGATACCCCTACGTGCGCTTCGCCGACCTCATGGGGTACATACCGCTCGTCGGCGCCC	769
Sbjct 710	CGATACCCCTACGTGCGCTTCGCCGACCTCATGGGGTACATACCGCTCGTCGGCGCCC	769
Query 770	TCTTGGAGGCCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAAAGACGGCTGAA	829
Sbjct 770	CTTGGGGCCCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAGGACGGCTGAA	829
Query 830	CTATGCAACAGGGAACCTTCTGGTGTCT-CTTCTCTATCTCTCTGGCCCTGCTCT	888
Sbjct 830	CTATGCAACAGGGATCTGCCGGTGTCTCTT-CTATCTCTCTTGGCTTGGCTGT	888
Query 889	CTTGCCCTGACTGTGCC-GCTTCAGCTACCAAGTGCACAA-T-TCCCTGGGGCTTAC	944
Sbjct 889	CTTGCCCTGACTGTGCC-GCTTCAGCTACCAAGTGCACAA-T-TCCCTGGGGCTTAC	944
Query 945	CATGTCACCAATGATTGC-CCTAACTCGAGTATTGTACGAGGGCGCCG--ATGCCATC	1001
Sbjct 945	CATGTCACGACGACTGCTCC-AACGCAAGCATGTGTAAGGGCACCGGACATG--ATC	1001
Query 1002	CTGCACACTCCGGGTGTGT-CCCTTGCCTTCGCAGGGTAACGCCCTCGAGGTGTTGGGT	1060
Sbjct 1002	ATGCATACCCCGGGTGCCTGCC-TGCCTCGGGAAACAACTCCCTCCGCTGCTGGGT	1060
Query 1061	GGCGGTACCCCCACGGTGGCACCAAGGGACGCGAAC-TCCCCAACCGCA-GCTTGA	1118
Sbjct 1061	AGGGCTCACTCCACGCTCGGCCAGGAAC-GCTAGCTCCCCACTACG-ACGATACGA	1118
Query 1119	CGTCATATCGATCTGTTGCGGGAGC-GCCACCCCTGCTCGGCCCTACGTGGGGGA	1177
Sbjct 1119	CGCCATGTCGATTGCTCGTGGG-GCGCTGCTCTGCTCCGCTATGACGTGGGGAGA	1177

Query	1178	CCTGTGGGGTCTGCTTT-CTTGTGGTCAACTGTTACCTTCTCTCC-CAGGGCCAC	1235
Sbjct	1178	TCTCTGGGATCTGT-TTCTCTGCGCCAGCTGTCACCTCTCCCTC-GCCGGCAC	1235
Query	1236	TGGACGAC-G-CAAGACTGCAATTGTTCTATCATCCCGGCCATATAACGGGTGATCGC	1292
Sbjct	1236	--GA-GACAGTACAGGACTGCAATTGTCATATATCCCGGCCAGTGCAGGGTCACCGT	1292
Query	1293	ATGGCATGGGATATGATGATGAACTGGTCCCCAACCGCAGCGTTGGTGTAGCTCAGCTG	1352
Sbjct	1293	ATGGCTTGGGATATGATGATGAACTGGTACCTACAGCAGCCCTAGTGGTATCGCAGTTA	1352
Query	1353	CTCGGATCCCACAAAGGCCATCATGGACATGATGCGCTGGTCTCACTGGGAGTCTGGG	1412
Sbjct	1353	CTCGGATCCCACAAAGCTGCTGGATATGGGGGGGGCCATTGGGAGTCTAGCG	1412
Query	1413	GGCATACGTA-TTCTCATGGGGAACTGGGAAAGGTCTGGTAGTGCTCTGCT	1471
Sbjct	1413	GGCTTGCCTACTAT-TCCATGGTGGGAACTGGGTAAGGTCTGATGTGATGCTACT	1471
Query	1472	ATTTCGGCGCTGACCGGAAACCCACGTACCCGGGAAATGCCGCC-GCACCGG	1530
Sbjct	1472	CTTTCGGCGCTTGACGGGAAACCTATGTGACAGGGG-GACGATGCCAAACAC-C	1529
Query	1531	CT-GGGCTTGTGTT-CTCTTACACCAAGGCCCA-AGCAGAACATCAAC-TGATCAA	1585
Sbjct	1530	CTCGGG-AT-TACGCCCTCTTACCCGG-GTCATCCCAAGAAATCCAGCTTG-TAAA	1585
Query	1586	CACCAACGGCAGTTGCCACATCAATAGCACGGCTTGAATGGCAATGAAAGCTTAAACAC	1645
Sbjct	1586	CACCAACGGCAGCTGGCACATCACAGGACTGGCTGAAGTCAATGACTCCCTAACAC	1645
Query	1646	-CGCGTGGTTAGCAGGGCTCTCTATC-AACACAAATTCAACTCTCAGGCTGCTCTGAG	1703
Sbjct	1646	TGGGTTCTT-GCTGCGTGTCTA-CGTGACAAGTCACATCTGGATGCCAGAG	1703
Query	1704	AGGTTGGCAGCTGCCACGCC-T-TACCGATTGGCCAGGGCTGGGCTCTATCAGTT	1761
Sbjct	1704	CGCATGGCAGCTCGAG-CCCCATCGA-CGGCTTCCCTAGGGTGGGGCCATCACTT	1761
Query	1762	ATGCCAACG-G-A-AGCGGCCCT-GACGA-ACGCCCTACTGCTGCCACTACCCCTCAA	1815
Sbjct	1762	A---CAATGAGTCACA-CAG-CTCGGACCGAGA-GGCCATTATGGTGGCACTACGCCACCC	1815
Query	1816	GACCTTGTGGCATTTGCCGCAAAG-ACGGTGTGGCCGGTATATGCTTCACTCCC	1874
Sbjct	1816	GGCGTGCCTATCTACCCGGGCCAG-GTGTGTGGTCACTGTAATGCTTCAAC-CCC	1873
Query	1875	-AGCCCCGTGGTGGGAACGACCCGACAGG-TCGGCG-CGCCCTACAGCTGGGT	1931
Sbjct	1874	AAAGCCCTGTGCTGGTGGGGACGACCCGACGGGTC-CGGCTC-CCTACGTACAGTTGGG-	1930
Query	1932	GCA-AATGATACGGATGT-CTTCGTCCTTAACACAC-CAGGCCACCGCTGGGCAATTGG	1988
Sbjct	1931	GGGAAATGAGACGGACGTGTCG-TCCTTAACACACGC-GGCCGCCAAGGCAACTGG	1988
Query	1989	TTCCGGTTGTAACCTGGATGAACCTCA---ACTGGATTACCAAAAG-TGTGC-GGAGGCCCCCC	2044
Sbjct	1989	TTTGGCTGTACATGGATGAA-T-AGCACTGGGTCAAC-AAGACGTGCGGGGC-CCCCC	2044
Query	2045	TTGTGTATCGGAGGGG-TGGCAACACACCTG-CTCTGCCCACTGATTGCTTCCG	2102
Sbjct	2045	GTGTAACATCGG-GGGGATCGGAAATAACACCTGAC-CTGCCACGGACTGCTTCCG	2102
Query	2103	AAACATCCGGAAGGCCACATACTCTC-GGIGCGCTCCGGCTCTGGATT-ACACCCAGGT	2160
Sbjct	2103	AACCAACCCGAGGGCCACCTACAC-CAAAGTGTGGTTCGGGCCCTGG-ITGACACCCAGAT	2160
Query	2161	GCATGGTCGACTACCCGATAGGCTTGGCACTATCTTGTACCATCAA-TTACACCAT	2219
Sbjct	2161	GCTGGTCCACTACCCATACAGGCTTGGCACTACCCCTGCACGTCAACTT-TACCATC	2219
Query	2220	TTCAAGGTAGGATGTACGTGGG-GGGAGTGGAGCACAGGCTCGAAGCCGATGCAATTG	2278
Sbjct	2220	TTCAAGGTAGGATGTACGTGGG-GGGAGTGGAGCACAGGCTCGAAGCCGATGCAATTG	2278

Query	2279	GACGCCGGGGCGAACGCTGTGATCTGGAAAGACAGGGACAGGTCCGAGCTCAGCCCGTTGCT	2338
Sbjct	2279	GACTCGAGGAGAGCGTGTAACTCTGGAGGACAGGGACAGATCAGAGCTTAGCCCGTCCT	2338
Query	2339	GCTGTCCACACACAGTGGCAGGTCTT-CCGTGTTCTTCAGCACCTGCCAGCT-TG	2396
Sbjct	2339	GCTGTCTACACAGGAGTGGCAGGT-ATTGCCCTGTCTCACCAACCTTACCGCTCTG	2396
Query	2397	TCCACCGGCTCATCCACCTCCACCAAGAACATTGGGACGTGCGAGTACTTGTACGGGTA	2456
Sbjct	2397	TCCACTGGTTGATCCATCTCATCAGAACGCTGTGGACGTACAAATACCTGTACGGTATA	2456
Query	2457	GGGTCAAAGC-ATCG-CGTCCTGGGCAATTAAAGTGGGAGTACGTGT-TCTCTGTCTT	2513
Sbjct	2457	GGGTC-GCCGGTTGTC-TCCTTGTCAATTAAAGTGGGAGTGTCTGT-TGCTCTCTT	2513
Query	2514	CTGCTTGAGACGGCCGGCTGTCT-CTCTGCTTGGAATGTGTACTCATATCCAAAGC	2572
Sbjct	2514	CTCTGGCCGAGCCGGCTGTCTG-TGCCCTGTCTTGGAATGTGTCTGTGATAGCTCAAGC	2572
Query	2573	GGAGGCGGCTTGAGAACCTCGTAATACTCAATGCAGCATCCTGGCCGGACGCAACGG	2632
Sbjct	2573	TGAGGCGGCTCATAGAACCTGTGTGGCTCAACGGGACATCGGTGGCCGGCGCAIGG	2632
Query	2633	TC-ITGCTGCTCTCTCTGTCTCTGTCTGCT-ITGCTGTTGATC-TGAAGGGTAGG-TGG	2688
Sbjct	2633	-CATTCCTCTCTCTCTGTCTCTGTCTG-TGCTGCTCTGTGATCAAGGGCAGCT-GG	2688
Query	2689	TGCCCT-GGAGGGTC-TACGCCCTTACGG-GATGTGGCTCTCTCTGCTCTGCTGG	2745
Sbjct	2689	T-CCCTGGGGCG-CATATGCCCTTACGGCG-TATGGCGTACTCTGCTCTGCTGG	2745
Query	2746	CGTTGCC-TCAGGGGCATACG-CACTGGACAC-GGAGGTGGCCGCCGTCGTGGCGGG	2802
Sbjct	2746	CGTTACCAACCA-CGAGCATACGCCA-TGGAC-CGGGAGATGGCAGCATCGTGGAGGG	2802
Query	2803	TTGTTCTT-GTCGGGT-TAATGGCGC-TGA-CTCTGTCGCCATATACAAGC-GCTAT-A	2856
Sbjct	2803	CGGTT-ITCGT-AGGTCTGAT-ACTCTTGACCT-TGTCACCGCACTATAAGCTG-T-TCC	2856
Query	2857	TCACTG-GG-TGCTGTTGGCTT-CAGTATTTCTGACCAGAGTAGAAGCGCA-AC-T	2911
Sbjct	2857	TC-GCTAGGC-TATATGGTG-TTACAATATTTTACACCAGGGCCG-AG-GCACACTT	2911
Query	2912	GCACGTGGGTTccccccctCAACGTCgggggggggggggggggggggggggggggggg	2971
Sbjct	2912	GCAAGTGTGGATCCCCCCCCCTAACCTTGGGGGGGGGGGGGGGGGGGGGGGGGGGG	2971
Query	2972	GTGTGTAG-TACACCC-GACCCCTGGTATTGTA-CATCACCAAACAC-TCCGGCCAT-C	3026
Sbjct	2972	GTGCG-CGATCCCCCAGA-GCTAATCTTT-ACCATCACCAAAT-CTTGTCTGCCATAC	3027
Query	3027	TTCCGGACCCCTT-TTGGATTCTCAAGCCAGT-TTGGCTTAAAGTCCCCACTTCGTGGCG	3084
Sbjct	3028	-TCCGTCCACTCATGG-TGCTCAGGCTGTGATAAC-CAAAGTGGCTACTTCGTGGCG	3084
Query	3085	TTCAAGGCCCTTC-TCCGGAT-C-TGGGGCTTAGCGGGAAAGATAGCGGGAGGTCTTACG	3141
Sbjct	3085	CACACGGGCTCATTC-G-TGCTGATGCTGGTGGGAAAGTGTGGCTGGGGTCTATTAG	3141
Query	3142	TGCAAATGGC-CATCATCAAGTGTAGG-GCCGCTTAAGTGGACCTATGTGATATAACCAT	3199
Sbjct	3142	TCCAAATGGCTC-TCATGAAGTT-GCCGCCACTGACAGGTACGTACCTTATGACCACT	3199
Query	3200	CACCCCTCTCGAGACTGGGCGACAAC-GGCCCTGGAGATCTGGCGTGGCTGTGAAAC	3258
Sbjct	3200	CACCCCACTGGGGACTGGGCCAC-GCGGGCTAACGAGACCTTGGCGTGGCAGTTGAGC	3258
Query	3259	CAGTCGCTCTCCCGA-ATGGAGACCAAGCTCATACGCTGGGGGGCAGATACCGCCCG	3317
Sbjct	3259	CCGTCGCTCTCT-CTGATATGGAGACCAAGGTATCACCTGGGGGCGAGACACCGCG	3317
Query	3318	TGCGGTGACATCATCAACGGCTTGGCGTCTCTGGCGTAGGGCCA-GGAGATACT-GTC	3375
Sbjct	3318	TGTGGGACATCATCTTGGCCTGGCGTCTCGCCCGCAGGGG-GAGGGAGATACT-C	3375

Query	3376	TTGGG-CCAGCCGAC-GGAATGGTCTCCAAGGGGTGAGGTTGCTGGCGCCCATCACGGC	3433
Sbjct	3376	-TGGGACGGCAGACAGCCTGAAGGGC-AGGGGTGGCAGTCTCCGGCTATTACGGC	3433
Query	3434	GTACGCCAGCAGACGAGGGCTCTAGGGTGTATAATCACAGCTGACTGGCGGGA	3493
Sbjct	3434	CTACTCCAAACAGAGCGGAGGCCTAATTGGCTGCATCATCACTAGGCTCAGGGCGGGA	3493
Query	3494	AAAAACCAACTGGAGGGTGGAGGTC-AGATCGTGTCAACTGCTACCCAAACCTTCCTGG	3552
Sbjct	3494	CAGGAACCAAGGTGAGGGGGAGGTCCAAG-TGGTCTCCACCGAACACAAATCTTCTGG	3552
Query	3553	CAACGTCCATCAATGGGTATGCTGACTGTCTACCAACGGGGCGGAGCAGGGACATCG	3612
Sbjct	3553	CGACCTGCGTCAATGGCGTGTGGTACTGTCTATCATGGTGGCGGCTAAAGAACCTTG	3612
Query	3613	-CATCACCCAGGGTCTGTATCCAGATGTATAACCAATGGACCAAGACCTTGTGGC	3671
Sbjct	3613	CCGGC-CCAAAAGGGCCAAATCACCCAAATGTACACCAATGTGGACAGGACCTGTGCGC	3671
Query	3672	TGGCCCCGCTCTCAAGGTTCCGCTCATGACACCTGTACCTGGCTCTCGGACCTT	3731
Sbjct	3672	TGGCAAGCGCCCCCGGGCGGTTCTGACACCATGACCCATGCGACAGCTCGGACCTT	3731
Query	3732	TACCTGGTACAGAGGCACGGCGATGTCATCCGTGGCGGGAGGTGATAGCAGGGGT	3791
Sbjct	3732	TACTTGGTACAGAGGCATGGCGATGTCATCCGTGGCGGGCGGAGCAGCAGGGGG	3791
Query	3792	AGCCCTGTTTGC----GGCCCCATTCTCCTACTTGAAAGGCTCTCGGGGGGCTCGCTGT	3850
Sbjct	3792	AGCCTACTCTC-CCCCAGGCCGTCTCTACTTGAAAGGCTCTCGGGCGGTCACTGCT	3850
Query	3851	GTGCCCGCGGGACACGCCGTGGC--CTATTCAAGGCCCGGGTGTGACCCGTGGAGTG	3908
Sbjct	3851	CTGCCCTCGGGGACCGTGTGGCATCT-TTC-GGGCTGCCGTGTCACCCGAGGGTT	3908
Query	3909	GCTAAAGCGTGGACTTAT-CCCTGTGGAGAACCTA-GG-GACAACCATGAGATCCCCG	3965
Sbjct	3909	GGCAAGGCCGTGGACTTGTACCC-GTCCAG--TCTATGAAACCACTATGCCGTCCCCG	3965
Query	3966	GTGTTACGGACAACCTCTCCACCAAGCAGTGGCCAGAGC-TCAGGGCCACCT	4024
Sbjct	3966	GTCCTACGGACAACCTGTCCTCCGGCGTACCCGAGA-CATTCCAGGTGGCCCATCT	4024
Query	4025	GCATGCTCCC-ACCGGCA CGGTAAAGGACCAAGGCTCCGGCTGCCTACCCAGCCC-AG	4082
Sbjct	4025	ACACGC-CCCTACTGTGACCGCAAGGACTAAGGTGCCGTGCTATGCAAGCCCAAG	4083
Query	4083	GGCTACAAGGTG-TTGGTGTCTAACCCCTCTGTTGCTGAAACGCTGGGCTT-GGTGCTT	4140
Sbjct	4084	GG-TATAAGGTGCTT-GTCCCTGAAACCGTCCGTGCCGGCACCTAGG-TTCCGGGGGT	4140
Query	4141	ACATGTCCAAGGCCATGGGGTGTCTTAATATCAGGACCGGGTGAGAACAAATTACCA	4200
Sbjct	4141	ATATGTCTAAGGCACATGGTATCGACCCCTAACATCAGAACCGGGTAAGGACCATCACCA	4200
Query	4201	CTGGCAG-C----CCCATCACGTACTCCACCTACGGCAAGTTCTTGGCGACGGGGGTGCTCA	4259
Sbjct	4201	C-GGGTGCCCCCATCACGTACTCCACCTATGGCAAGTTCTTGGCGACGGGTGGTGTCT	4259
Query	4260	GGAGGTGCTTATGACATAATAATTGTGACGAGTGCCACTCCACGG-TGCCA-CATCCA	4317
Sbjct	4260	GGGGGCCCTATGACATCATATAATGTGATGAGTGCCACTCAACTGACT-CGACCA-CTA	4317
Query	4318	TCTGGGCATCGGACTGTCTTGGACCAAGCAGAGACTGCGGGGGCAGACTGGTGTGC	4377
Sbjct	4318	TCTCTGGGCATCGGACACACTCTGGACCAAGCGGAGCGGTGGAGCCGACTCTGTGTC	4377
Query	4378	TGCCCACTGCTACCCCTCGGGCTCGTCACTGTGTC-CATCTAACATCGAGGAGGT	4436
Sbjct	4378	TCGCCACCGCTACGCCCTCGGGATCGGTACCGTG-CCACATCCAAACATCGAGGAGGT	4436
Query	4437	GCTCTGTCACCCACGGAGAGATCCCTTTAGGGCAAGGCTATCCCCCTGGAGGTGATC	4496
Sbjct	4437	GCTCTGTCACGGAGAAATCCCTTTATGGCAAGCCATCCCCATCGAGACCATC	4496

Query	4497	AAGGGGGGAAGACATCTCATTTCTGCCACTCAAAGAAGAAGTGCAGCGAGCTGCCCGC	4556
Sbjct	4497	AAGGGGGGAGGCACCTCATTTCTGCCATTCAAGAAGAAATGTGATGAGCTGCCCGC	4556
Query	4557	AAGCTGGT-C-GCATTGGGCATCAATGCCGTGGCTACTACCGGGCTTGACGTGTCG	4614
Sbjct	4557	AACT-GTCCGGCTCGGAC-TCAATGCTGTAGCATATTACCGGGCTTGATGTATCCG	4614
Query	4615	TCATCCCGACCAGGGCGATGTTGTCGTGTCGACCTGGCTT	4673
Sbjct	4615	TCATACCAACTAGCGGAGACGTATGTCGTAG-CAACGGACGCTCTAATGACGGGCTT	4673
Query	4674	ACCGGCAGCTTCGACTCTGTGATAGACTCCAACACGTGTCGACTCAGACAGTCGATT	4733
Sbjct	4674	ACCGGCAGTTTCGACTCAGTGACTGCAATACATGTCACCCAGACAGTCGACTTC	4733
Query	4734	ACGCTTACCCCTACCTTACCATTTGAGACAAACCA-CGCTCCCCAGGATGCTGTC-CA-	4791
Sbjct	4734	ACGCTTGACCCGACCTTCACCATTTGAGACGACGACCG-TCGCCACAAAGACGGGTG-CAC	4791
Query	4792	GGACTAACGCCGGGGCAGGACTGGCAGGGGAAGCCAGGCATCTATAGATTGTCAC	4851
Sbjct	4792	GCTCGCAGCGGGAGGGCAGGACTGGTAGGGCAGGATGGCATTACAGGTTGACTC	4851
Query	4852	CGGGGGAGCGCCCCCTCCGGCATGTTGACTCGTCCCTCTGTGACTGCTATGACGGG	4911
Sbjct	4852	CAGGAGAACGGCCCCCTCGGGCATGTTGATTCCTCGGTTCTGTGCGACTGCTATGACGGG	4911
Query	4912	GCTGTGCTTGGTATGAGCTCACGCCCGGGAGAC-TACAGTTAGGCTACGAGCCTACATG	4970
Sbjct	4912	GCTGTGCTTGGTACGAGCTCACGCCCGGGAGACCT-CAGTTAGGTTGCGGGCTTACCTA	4970
Query	4971	AACACCCCCGGGCTT-CCCGTGTGCCAGGACCATCTTGAAATTGGAGGGCTTTAC	5029
Sbjct	4971	AACACACCAAGGG-TTGGCCGCTGCCAGGACCATCTGGAGTTCTGGAGAGCGCTTTAC	5029
Query	5030	GGGCCCTACTCATATAGATGCCACTT-TTATCCAGACAAAGCAGAGTGGG-GAGAAC	5087
Sbjct	5030	AGGCCCTACCCACATAGACGCCA-TTCTTGCTCCAGACTAAAGCAG-GCAGGAGAAC	5087
Query	5088	TTTCCCTACCTGGTAGCGTACCAACGCCACCGTGTGCCCTAGGGCTAACGCCCTCCCCCA	5147
Sbjct	5088	TTTCCCTACCTGGTAGCATACCAGGCTACGGTGTGCCAGGGCTCAGGCTCCACCTCCA	5147
Query	5148	TCTGGGGACCAAGATGGAAGTGTGATCGCTTAAACCC-ACCCCTCATGGGCAAC	5206
Sbjct	5148	TCTGGGGACCAAAATGGAAGTGTCTACAGCT-AAAACCTACGGTGCACGGGCAAC	5206
Query	5207	ACCCCTGCTATACAGACTGGCGCTGTTAGAATGAAGTCAC--CCTGACGCACCCATC	5264
Sbjct	5207	GCCCTGCTGTATAGGCTGGAGGCCGTTCAAACAGGGTTACTACC--ACACACCCATA	5264
Query	5265	ACCAAATACATCATGACATGTCGGCCGACCTGGAGGTGTCACAGAGCACCTGGGT	5324
Sbjct	5265	ACCAAATACATCATGGCATGTCGGCTACCTGGAGGTGTCACAGAGCACCTGGGT	5324
Query	5325	CTGTTGGCGCGCTCTGGCTGCTGGCCGCTATTGCTGTCAACAGGCTGGCTGTC	5384
Sbjct	5325	CTGGTAGCGGGAGCTCTAGCAGCTGGCCGCTATTGCTGTACAACAGGCTGGTC	5384
Query	5385	ATAGTGGGCAGGGATGTCCTTGCCGGAAAGCCGCATTATACCTGACAGGGAGGTTCTC	5444
Sbjct	5385	ATAGTGGGCAGGGATCATCTGTCGGAAAGCCGCATCATCCGCACAGGGAGTCCT	5444
Query	5445	TACCAAGGAGTTCGATGAGATGGAAGAGTGTCTC-TCACGACTTACCGTACATCGAGCAAG	5503
Sbjct	5445	TACCCGGAGATTCGATGAGATGGAAGAGTGTGCGCTCA-CACCTCCCTACATCGAACAGG	5502
Query	5504	GA-TG-ATGCTCGCTGAGCAGTTCAAGCAGAAGGCCCTGGCTCTGCAGACGGCGTCC	5561
Sbjct	5503	GAATGCA-GCTCGCGAACAAATCAACAGAAGGCAATCGGGTGCTCAAACAGCCACC	5561
Query	5562	C-GCCATGAGGGTTA-T-CACCCCTGCTGTCAGACACCAACTGGCAAAACTCGAGGT	5618
Sbjct	5562	AAGCAA-GCGGAGGCTGCTGCCGTGGTGA-AT-CCAAGTGGGGACCCCTCGAAGCC	5618

Query	5619	TTTGGGCGAAGCACATGTGAATTCATCAGTGGATAACAATACTTGGCGGGCTGTCA	5678
Sbjct	5619	TTCTGGGCGAAGCATATGTGAATTCATCAGCGGATAACAATATTAGCAGGCTTGTCC	5678
Query	5679	ACGCTGCCTGGTAACCCCGCCATTGCTTATTGATGGCTTACAGC-TGCCGTACCAAG	5737
Sbjct	5679	ACTCTGCTGGCAACCCCGCATAGCATCACTGATGGCATTACAGCCT-CTATCACCAAG	5737
Query	5738	CCCACTAACCACTGGCAAACCTCTCTTCAACATATTGGGGGGGGGGGGGGGGGGGGGG	5797
Sbjct	5738	CCCCTCACCAACCATACCCCTCTGGTTAACATCTGGGGGGGGGGGGGGGGGGGGGG	5797
Query	5798	GCTGGCGGCC-CCCGGTGCCGTACTGCTT-TGTTGGGTCTGGCTTAGCTGGCGCCGCC	5855
Sbjct	5798	ACTTGCT-CCTCCAGCGCTGCTTGC-TTCTGTAGGCGCCGGCATCGCTGGAGCGCT	5855
Query	5856	ATCCGGCAGCGTTGACTGGGAAGGTCTCTGTGGACATCTTG-CAGGGTATGGGG-GG	5913
Sbjct	5856	GTTCGGCAGCATAGGCCCTGGGAAGGTGCTTGTGGATATT-TTGGCAGGGTATGGAGCAGG	5914
Query	5914	GCGTGGGGGGAGCTTGTAGCATCAAGATCATGAGCGGTGAGGTCCCCCTCCACGGAGG	5973
Sbjct	5915	G-CTGGCAGGCCGCTGTGGCTTAAAGGTATGAGCGGCAGAGATCCCCCTCACCGAGG	5973
Query	5974	ACCTGGTCAATCTGCTGCC-GCCATCCCTCTGCCCTGAGCCCTTGATGCGGTGTGGTC	6032
Sbjct	5974	ACCTGGTAAACCTACT-CCCTGCTATCCCTCTCCCTGGCCCTAGTCGTGGGGTCGTG	6032
Query	6033	TGGCGAGCAAATCTGGCGGGCACCTTGGCCC-GGGGGAGGGGGCAGTGAATGGATGAA	6091
Sbjct	6033	TGCGCAGCGATACTGCGTCGGCACCTGGGGCCAGG-GAGGGGGCTGTGCACTGGATGAA	6091
Query	6092	CCGGCTAATAGCCTCGCCTCCGGGGAAACATGTTCCCCACGCACTACGTGGCGGA	6151
Sbjct	6092	CCGGCTGATAGCGCTTGCCTGGGGTAACACGCTCCCCACGCACTATGTGCGTGA	6151
Query	6152	GAGCGATGAGCCGCCCGTCACTGCA-TACTCGC-AGCCTACTGTAAACCCAGCTC	6209
Sbjct	6152	GAGCGAGCGTCGAGCACCGTCACT-CAGATCTCT-CTAGTCTACCATCACTAGCTG	6209
Query	6210	CTGAGGGCAGTCAGTGGAT-AAGCTGGAGT-TACCACTCATGCTCCGGTTCT	6267
Sbjct	6210	CTGAAGAGGGCTCACCACTGGATCAA-CGAGGACTGCT-CCACGCTATGCTCCGGCTCGT	6267
Query	6268	GGCTAAGGGACATGGGACATGGATATGGGA-GGTGCTGAGC-GACTTT-AAGACCTGGC	6324
Sbjct	6268	GGCTAAGAGATTTGGATGGATATGC-ACGGTGTGA-CTGA-ITTCAGAACCTGGC	6324
Query	6325	TGAAAG-CCAAGCTCATGCCACAATGCTGGGATTCCTTGTGC-C-TGCCAGCGCG	6381
Sbjct	6325	TCCA-GTCCAAAGCTCTGCCGGATGCC-GGGAGTCCTCT-TCTCATGTCAACCGT	6381
Query	6382	GGTATAAGGGGGCTGGCGAGGAGACGGCATTATGCACACTCGC-TGCC-ACTGTGGAGC	6439
Sbjct	6382	GGTACAAGGGAGTCGGGGGGCGACGGCATATGCAAAC-CACCTGCCA-TGTGGAGC	6439
Query	6440	TGAGATCACTGGACATGCAAAACGGGACGATGAGGGATGTCGGCTTAGGACCTGAG	6499
Sbjct	6440	ACAGATACCGGACATGTGAAAACGGTTCATGAGGATGTCGGGGCTAGGACCTGTAG	6499
Query	6500	GAACATGTGG-AGTGGGACGTCCCCATTAAACGGCTACACCAACGGGGCCCTGTACTCCCC	6558
Sbjct	6500	TAACACGTGGCA-TGGAACATCCCCATTAAACGGTACACCAACGGGGCCCTGCACGCC	6557
Query	6559	TCCTG-CGCCGAACTATAAGTCG-CGCTGTGGGGGTGTCTGCAGAGGAATACGTGGA	6616
Sbjct	6559	TCCCCGGCGCCAAATTATTC-TAGGGCGCTGTGGGGGTGTCTGAGGGAGTACGTGGA	6616
Query	6617	GATAAGGGGGGGGGGGACTTCACTACGT-ATCGGGTATGACTACTGACATCTAA-	6674
Sbjct	6617	GGTACCGGGGGGGGGATTTCACTACGTGA-CGGGCATGACCAACTGACAA-CGTAAG	6674
Query	6675	TGCCCGTGGCACAGATCCCATCGCCGAATTTCACAGAATGGACGGGGTGCCTACAC	6734
Sbjct	6675	TGCCCGTGTCAAGTCCGGCCCCGAATTCTCACAGAAGTGGATGGGGTGCCTACAC	6734

Query	6735	AGGTTTGC...GGGGAGGAGGT-ATCATTCA-GAGTAGGAC	6792
Sbjct	6735	AGGTACGCTCCAGCGTGC...ACGGAGGGTCA-CATTCTG-GTCGGC	6792
Query	6793	TCCA-CGAGTACCGGTGGGTGCGAATTACCTTGC...GACCGAGCTAGCGTG	6851
Sbjct	6793	TCAATCAA-TACCTGTGTTGGTCACAGCTCCCATGGGAGGCCA...GCTAGCTG	6851
Query	6852	TTGACGTC...CATGCTCACTGATCCCACATATAACAGCAGAGGCCGGGGAGAAGTTG	6911
Sbjct	6852	CTCACTTCATGCTCACCGACCCCTCCACATTACGGCAGAGCGGCTAACCGTAGGCTG	6911
Query	6912	GCGAGAGGG-TCACCCCTTC-TATGGCCAGCTCTCGGCTAGCCACGTGTCGCTCCAT	6969
Sbjct	6912	GCCAG-GGGATCTCCCCCTCTT-TGGCCAGCTCATCAGCTAGCCAGCTGTCTGCCCT	6969
Query	6970	CTCTC-AAGGCAACTTGACCGCAACCATGACTCCCTGACGCCAGCTCATAGAGGT	7028
Sbjct	6970	C-CTTGAAAGCAACATGCACTACCCGTATGACTCCCCGACGCTGACCTCATCGAGGCC	7028
Query	7029	AACTCTGTGGAGGCAGGAGATGGGCGCAACATACCAGGGTTGAGTCAGAGAACAAA	7088
Sbjct	7029	AACTCTGTGGCGCAGGAGATGGGCGGGAAACATACCACGTGGAGTCAGAAAATAAG	7088
Query	7089	GTGGTGA...CTGGACTCTTCGATCCGCTGTGCGAGAGGAGATGAGCGGGAGGTC	7148
Sbjct	7089	GTAGTAATTGGACTCTTCGAGCGCTCAAGCGAGGAGGATGAGAGGGAAAGTATCC	7148
Query	7149	GTAACTGCAGAAATCTGGAAAGTC-GGAGATTGCC-...CGGGCCCTGCCGTCTGG	7206
Sbjct	7149	GTTCCGGGGAGATCTCGCGAGGTG-CAGGAATTTC-CTCGAGCGATGCCATATGGG	7206
Query	7207	CGCGCCGGACTACAACCCCCCGCTAGT-AGAGACGTGGAAAAGCCTGACTACGAACCA	7265
Sbjct	7207	CACGCCCGGATTACAACCTCCACT-GTAGAGTCTGGAAAGGACCCGGACTACGTCCT	7265
Query	7266	CCTGTGGT...CATGGCTGCCGCTACCACT-CCACGGTCCCCTCTG-TGCCCTCC	7323
Sbjct	7266	CCAGTGGTACAGGGTGCATTGCCGCTGCCAAGG-CCCCTC-GATAACCACTCCAC	7323
Query	7324	GGAAAAAGCGTACCGGTGGCTCTACCGAATCACCTATCTACTGCC...GGCTTG	7383
Sbjct	7324	GGAGGAAGAGGACGGTTGCTCTGTCAGAATCTACCGTGTCTCTGCC...GGAGCTCG	7383
Query	7384	CCACCAAA-AGTTTGGCAGCTCTCAA-CTTCGGCATT--ACGGGGACAATACGACA	7439
Sbjct	7384	CCAC-AAGACCTTCGGAGCTCCG-AATGTC-GGCCGTGACAG-CGGCA---CGGCA	7436
Query	7440	ACATCCCTG...A-GCCC-GCCCTCTG-G-CTGcccccccG-AC...CCGACTG	7493
Sbjct	7437	ACGGCCCTCTCTGACCAAGCCC-TCC-GACGACGGGACGCCGA-TCCGACGTGAGTCG	7493
Query	7494	TATTCTCCATGGcccccccTGGAGGGGGAGCCTGGGATCTCGGACGGGTCA	7553
Sbjct	7494	TACTCCCTCATGCC...CCCTTGAGGGGGAGCGGGGATCCGATCTCAGCGACGGGTCT	7553
Query	7554	TGGTCGACGGTCA...GAGTGG-GGCCGACACGGAAGATGTCGTGCTGCTCAATGCTTA	7612
Sbjct	7554	TGGTC...TACCGTAAGC-GAGGAGGCT-AGT-G-AGGACGTGCTGCTGCTCGAAGTCTTA	7609
Query	7613	TTCC...GACAGGGC...ACTCG-TCACCCCGTGCCTGGGAAGAA-CAAAACTGCCATC	7670
Sbjct	7610	CACATGGACAGGCCCT-GATCACGCCATGGCTCGGGAGGAACCAAG-CTGCCATC	7667
Query	7671	AACGCACTGAGCACTCGTGTGCTACGCCATCACAACT-GGTGTATCCACCACTCAGC	7729
Sbjct	7668	AATGCACTGAGCAACTTGTGCTGCCATCACAA-CTGGTCTATGCTACAACATCTG	7726
Query	7730	CA...GTGCTGCCAAAGGAGAAGAAAGTCACATTGACAGACTGCAAGTCTGGAC-AGCC	7788
Sbjct	7727	CAGCGCAAGCGTGGCGAGAAGGTCACCTTGACAGACTGCAAGTCTGGACGA-CC	7785
Query	7789	ATTACCAAGGAGCTGCTCAAGGAGGTCAAAGC-AGCGGGCTCAAAGTGAAGGCTAA-CTT	7846
Sbjct	7786	ACTACCGGGAGCTGCTCAAGGAGATGAAGGC...AAGCTTAAGGCTAAACTT	7844

Query	7847	GCTATCCGTAGAGGAAGCTTGCA-GCCTGACCCCCCACATTAGCCAAATCCAAGTTG	7905
Sbjct	7845	-CTATCCGTGGAGGAAGCTGTAAAGC-IGACCCCCCACATTGGCCAGATCTAAATTG	7902
Query	7906	GCTATGGGCAAAAGACGTCGTTGCC-ATGCCAGAAAAGCCGT-AGCCACATCAACTC	7963
Sbjct	7903	GCTATGGGCAAAAGACGTCGTTGCCACCTAT-CCAGCAAGGCCGTAAACC-ACATCGCTC	7960
Query	7964	CGTGTGGAAAGACCTT-CTGGAAGACAGTGTAAACCAATAGACACTACCATCATGGCC	8021
Sbjct	7961	CGTGTGGAAAGGAC-ITGCTGAAAGACACTG-AGACACCAATTGACACCCACATCATGGCA	8018
Query	8022	AAGAACGAGGTTTCTGGGTTCAAGCTGAGAAGGGGGCTGTAAAGCCAGCTCGTCATC	8081
Sbjct	8019	AAAAATGAGGTTTCTGGCTCAACAGAGAAGGGGGCCGAAGCCAGCTCGCCATTAC	8078
Query	8082	GTGTTCCCCGACCTGGGCTGGCGTGTGGAGAAGATGGCCCTGTACGACGTGGT-TAG	8140
Sbjct	8079	GTATCCCCAGATTGGGGTTCGTGTGCGAGAAAATGCCCTTACGATGTGGTCTC-	8137
Query	8141	CAAGCTCCCCCTGGCGTGTAGGGAAAGCTCC-TACGGGATTCAACTACTCACCAGGACAGC	8199
Sbjct	8138	CACCCCTCCCTCAGGCCGTGATGGCT-CTTCATACGGGATTCAACTACTCTCTGGACAGC	8196
Query	8200	GGGTTGAATTCTCGTGCAGA-GCGTGGAA-GTCCAAAGAAC-CCCGATGGGGTTCTCGT	8256
Sbjct	8197	GGGTCGAGTTCTGGTGTAGCTGGAAAG-CGAAGAA-ATGCCCTATGGCTTCGAT	8253
Query	8257	ATGATACCCGCTGTTTGACTCCACAGTCACTGAGAGCCACATCCGTACGGAGGAGGCAA	8316
Sbjct	8254	ATGACACCCGCTGTTTGACTCAACGGTCACTGAGAATGACATCCGTGTTGAGGAGTCAA	8313
Query	8317	TTTACCAATGTTGTGACCTGGACCCCCC-AAGCCCG-CGTGGCATCAAG-TCCCTACTG	8373
Sbjct	8314	TCTACCAATGTTGACTTGG-CCCCCGAAGCCAGACA-GGCCAT-AAGGTGCTCACAG	8370
Query	8374	AGAGGCTTTATGTTGGGGCCCTTACCAATTCAAGGGGGAAAATCGGGCTACCGC	8432
Sbjct	8371	AGCCGCTTACATCGGGGGCCCCCTGACTAATTCTAAAGGGC-AGAACTGGGCTATCCG	8429
Query	8433	AGGTGCGCGCGAGCGCGTACTGACAACACTAGCTGGTAAACACCCCTACCTGCTACATC	8492
Sbjct	8430	CGGTGCGCGCGAGCGGTGACTGACGACAGCTGGTAAATACCCCTACATGTTACTTG	8489
Query	8493	AAGGCC-CGGGCAGCCTGTCGAGCCCG-AGGGCTCAGGACTGCACCATGCTGTGTG	8550
Sbjct	8490	AAGGCCCTG-CGGCTGTGAGCTGGAAAG-CTCAGGACTGCACATGCTCGTATCCG	8547
Query	8551	GCGACGAC-TTAGTCGTTATCTGTGAAAGTGCAGGGGTCAGGAGGACGCCGAGCTG	8609
Sbjct	8548	GAGACGACCTT-GTCGTTATCTGTGAAAGCAGCGGGGACCCAAGGGACGAGGCCGAGCT	8605
Query	8610	A-GAGCCTTACGGAGGCTATGACCAAGGTACTCCGCCCTCCCCCGGAGACCC-CCACACAAAC	8667
Sbjct	8606	ACGGGCTTACGGAGGCTATGACTAGAATCTGCCCCCCCCTGGGACCCGCCA-AAC	8664
Query	8668	CAGAATACGACTTGGAGCTT-ATAACATCATGCTCTCCAACTGTGTCAGTCGCCAACGAC	8726
Sbjct	8665	CAGAATACGACTTGGAG-TTGATAACATCATGCTCTCCAACTGTGTCAGTCGCCAACGAT	8723
Query	8727	GGCG-CTGG-AAGAGGGTCTACTACCTTACCCGTGACCCCTAACACCCCTCGGAAGAG	8784
Sbjct	8724	G-CATCTGGCAAAGGGTACTATCTACCCGTGACCCACACCCCTCGGGGG	8781
Query	8785	CCCGGTGGGAGACAGCAAGACACACTCCAGTCATTCCTGGCTAGGCAACATAATCATGT	8844
Sbjct	8782	CTGGGTGGGAGACAGCTAGACACACTCCAGTCATTCCTGGCTAGGCAACATCATGT	8841
Query	8845	TTGCCCTTACACT-GTGGCGAGGATGATACTGATGACCCATTCTT-TAGCGTCCT-CA	8901
Sbjct	8842	ATGCGCCAC-CTTGTGGCAAGGATGATCTGATGACTCATTTCTCTC-CATCTTC	8898
Query	8902	TAGC-CAGGGATCAGCTGAAAGCGCTTAA-ACTGTGAGATCTACGGAGGCTGCTACTC	8959
Sbjct	8899	TAGCTCAGGAA-CAACTGAAAAGCCCT-AGATTGTCAGATCTACGGGCTGTTACTC	8956

Score = 3354 bits (1816), Expect = 0.0
Identities = 3942/4944 (79%), Gaps = 244/4944 (4%)
Strand=Plus/Plus

Query 1	GCCAGCCCCCTGA-TGGGGGCAGACACTCCACCATGA-ATCACTCCCTGTGAGGAACATAC	58
Sbjct 1	GCCAGCCCCC-GATTGGGGCAGACACTCCACCAT-AGATCACTCCCTGTGAGGAACATAC	58
Query 59	TGTCTTCACCGCAGAACGCTAGCCATGGCTTAGTATGAGTGTCTGAGCCTCCAGG	118
Sbjct 59	TGTCTTCACCCAGAACGCTAGCCATGGCTTAGTATGAGTGTCTGAGCCTCCAGG	118
Query 119	AcccccccccTCCCGGGAGAGCCATAGTGGCTGGGAACCGGTAGTACACCGGAATTGCC	178
Sbjct 119	ACCCCCCCCCTCCGGGAGAGCCATAGTGGCTGGGAACCGGTAGTACACCGGAATTGCC	178
Query 179	AGGACGACGGGGTCTTCTGGATAACCCGCTCAATGCCCTGGAGATTGGCGTGC	238
Sbjct 179	AGGACGACGGGTCTTCTGGATCAACCCGCTCAATGCCCTGGAGATTGGCGTGC	238
Query 239	CCGCAAGACTGTAGCCGAGTAGTGTGGCTGGGAACGGCTTGTGGTACTGCCGTATA	298
Sbjct 239	CCGCGAGACTGTAGCCGAGTAGTGTGGCTGGGAACGGCTTGTGGTACTGCCGTATA	298
Query 299	GGGTGCTTGCAGTGGCCGGGGAGTCTCGTAGACCGTGACCATGAGCACGAATCTAA	358
Sbjct 299	GGGTGCTTGCAGTGGCCGGGGAGTCTCGTAGACCGTGACCATGAGCACGAATCTAA	358
Query 359	ACCTCAAAGAAAACCAAACGTAAACCAACCGTCGCCACAGGACGTCAAGTCCGGG	418
Sbjct 359	ACCTCAAAGAAAACCAAACGTAAACCAACCGTCGCCACAGGACGTCAAGTCCGGG	418

Query	419	TGGCGGTACAGATCGTGGTGGAGTTACTTGTGCGCGCAGGGGCCCTAGATGGGTGT	478
Sbjct	419	CGTGGTCAGATCGTGGTGGAGTTACTTGTGCGCGCAGGGGCCCTAGGTGGGTGT	478
Query	479	GCGCGCAGGAGAAAGACTTCCGAGCGGTCGCAACCTCGAGGTAGACGTAGCCCTATCCC	538
Sbjct	479	GCGCGCAGGAGAAAGACTTCCGAGCGGTCGCAACCTCGTGGAAAGGCACACCTATCCC	538
Query	539	CAAGGACGTGCGGCCAGGGCAGGACCTGGCTCAGCCGGTACCCCTGGCCCTCTA	598
Sbjct	539	CAAGGCTGCCAGGGCAGGGTAGGCCCTGGCTCAGCCGGTACCCCTGGCCCTCTA	598
Query	599	TGCAATGAGGG-TGCGGGTGGCGGATGGCTCTCGTCTCCCGTGGCTCTCGCCCTA	657
Sbjct	599	TGCAATGAGGGCTTG-GGGTGGCAGGATGGCTCTCGTACCCGTGGCTCTCGCCCTA	657
Query	658	GCTGGGCCACAGACCCCCCGCGTAGGTGCGCAATTGGTAAGGTATCGATACCC	717
Sbjct	658	GTGGGCCACAGACCCCCCGCGTAGGTGCGCAATTGGTAAGGTATCGATACCC	717
Query	718	TTACGTGCGGTTCCGCGACCTCATGGGTACATACCGTCGCGGCCCTCTGGAG	777
Sbjct	718	TCACGTGCGGTTCCGCGATCTCATGGGTACATACCGTCGCGGCCCTCTGGGG	777
Query	778	GCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAAAGACGGCGTGAACATATGCAA	837
Sbjct	778	GCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAGGACGGCGTGAACATATGCAA	837
Query	838	CAGGGAACCTCTCGTTGCTC-TTCTCTAATCTCTCTGGCCCTGCTCTTGCTG	896
Sbjct	838	CAGGGAACTCGCCCGTTGCTCTT-TCTATCTCTTTGGCTTGCTGCTCTTG	896
Query	897	ACTGTGCC-GCTTCAGCTACCAAGTGCCTAAT-TCTCGGG-GCTTACCAATGCA	953
Sbjct	897	ACCAT-CCCACTTCGCTTGAAGTGGCAACGTA-TCCGGAG-TGTACCAATGTCAG	953
Query	954	AATGATTGC-CCTAACCTGAGATTGTGTAACGAGGGGGCGA-TGCCATCTGCACACT	1010
Sbjct	954	AACGACTGCTCC-AACGCAAGCATGTGATGAGGCAGCGGACATG--ATCATGCATAC	1010
Query	1011	CCGGGGTGTGT-CCTTCGCTCGGAGGGTAACGCCCTGAGGTGTTGGTGGCGGTGAC	1069
Sbjct	1011	CCGGGGTGTGCTCC-CGCTTCGAGAACACTCTCCGCTGCTGGTAGCGCTCAC	1069
Query	1070	CCCCACGGTGCCACAGGAGGGAAAC-TCCCCAACAG-CAGCTTCGACGTCTATTC	1127
Sbjct	1070	TCCCCACGCTCGCCAGGAACG-CTAGCGTCCCCACTACGAC-GATACGACGCCATGTC	1127
Query	1128	GATCTGCTTGTGGAGCGCCACC-CTCTGCTGGGCCCTACGTGGGGGACCTGTGGG	1186
Sbjct	1128	GATTGCTCGTGGG-GCGGCTGCTCTGCTCGCTATGACGTGGAGATCTGGGG	1186
Query	1187	GTCGTCTTCTT-GTTGGTCACTGTTACCTCTCTCC-CAGGGCCACTG-GACGAC	1243
Sbjct	1187	ATCTGT-TTCCTCGCTGCCAGCTGTTACCTCTCGCTC-GCCGGCAC-GAGAC-A-	1241
Query	1244	GCA-AG-ACGTCAATTGTCTATCTATCCGGCCATATAACGGGTATCGCATGGCATGG	1301
Sbjct	1244	GTACAGGACTGCAATTGCTCAATATATCCGGCCACGTGACAGGTACCGTATGGCTGG	1301
Query	1302	GATATGATGTAACGGTCCCCACGGCAGGGTGGTGAACCTGCTCGGATC	1361
Sbjct	1302	GATATGATGTAACGGTACCTACAGCAGGCCATGTTACGCACTCCGGATC	1361
Query	1362	CCACAAGCCATCATGGACATGATCGCTGGTGTCACTGGGAGTCTGGCGGGCATAGCG	1421
Sbjct	1362	CCACAAGCTGCTGGATGTTGGCGGGGGCCATTGGGAGTCTAGCGGGCTTGG	1421
Query	1422	TATT-TCTCATGGTGGGAACTGGCGAACGGTCTGTAGTGTCTGTGCTATTGGCGG	1480
Sbjct	1422	TACTAT-TCCATGGTGGGAACTGGCTAAGGTCTGTTGATGATGCTACTCTTGCGCG	1480
Query	1481	CGTCAAGCGGAAACCCACGTACCGGGGGAAATGCCGGCCGAC-CACGGCT-GGGCT	1538
Sbjct	1481	CGTTGACGGGGACCTATGTGACAGGGGGAC-GATGGCAAAACACC-CTCGGGATT	1538

Query	1539	—GTTGGTCTCTTACACCAGGCCAAGC—AGAACATCCA—GATCAACACCAACGG	1594
Sbjct	1539	ACGTCCTCTT—TT—CACCCGG—GTCACTCCAGAAATCCAGCTTG—TAAACACCAACGG	1594
Query	1595	CAGTTGGCACATCAATAGCACAGGCCCTGAAATTGCAATGAAAGCCTTAACACGGCTGG—T	1653
Sbjct	1595	CAGCTGGCACATCAACAGGACTGCCCTGAACTGCAATGACTCCCTCACACTGGGTTCT	1654
Query	1654	TAGCAGGGCTCTTCTATCAA—CACAAATTCAACTCTTCAGGGCTGAGAGGTTGGCC	1712
Sbjct	1655	T—GCTGCGCTGTTCA—CGTGCACAAGTCAACTCATCTGGATGCCAGACCGCATGGCC	1712
Query	1713	AGCTGCGGAGCCCTT—AC—CGATTITGCCAGGGCTGGGGTCTATCAGTTATGCCAAC	1769
Sbjct	1713	AGCTGCAGCC—CCATCGACGCG—TTC—GCTCAGGGTGGGGGCCATCACTTA—C—AAT	1766
Query	1770	G—G—A—AGCGGCCCTCG—ACGA—ACGCCCTACTGTCGGACTACCCCTCAAGACCTGT	1823
Sbjct	1767	GAGTCACA—CAGC—TCGGACAGAGGCC—TATTGTTGGACTACGCACCCGGCGTGC	1823
Query	1824	GGCATTTGCCCCGAAAG—AGCGTGTGTTGGCCGGTATAATGCTTCACTCCCA—GCCCCG	1881
Sbjct	1824	GGTATCGTACCCGGCGCCAG—GTGTTGTTCCAGTGTACTGCTTCAC—CCCCAACCTG	1881
Query	1882	TGGTGGTGGGAAACGACCGACAGGT—CGGGCG—CGCCCTACCTACAGCTGGGGTGC—AATG	1938
Sbjct	1882	TCCGGGTGGGACCGACCGGGTTCGG—CGTC—CCTACAGTACAGTTGGGGG—AGAATG	1938
Query	1939	ATACGGATGT—CTTGTCTTAAACACAC—CAGGCCACCGCTGGCAATTTGGTTGGT	1996
Sbjct	1939	AGACGGACGTCTGTTTC—TTAACACACGCC—GGCCCGGCCAAGGCACTGGTTGGCTG	1996
Query	1997	TACCTGGATGAACT—CAACTGGATTACCAA—AGTGTGGGAGGCCCTTGTG—T—C	2051
Sbjct	1997	TACATGGATGAA—TAGCA—CTGGGTTACCAAGAC—GTGGGGG—GCCCCC—GTGTAAAC	2051
Query	2052	ATCGGAGGGG—TGGGCAACAACACTTG—CTCTGCCCACTGATTGTTCCGAAACATC	2109
Sbjct	2052	ATCGG—GGGATCGGCAATAAACCTTGAC—CTGCCCAACGGACTGTTCCGGAAAGCACC	2109
Query	2110	CGGAAGGCCACATACTCTCG—GTGCGGCTCCGGCTCTGGATT—ACACCCAGGTGCAATTG	2167
Sbjct	2110	CCGAGGCCACTACAC—CAAGTGTGTTGGGGCTTGG—TTGACACCCAGATGTTGGT	2167
Query	2168	CGACTACCGTATAGGCTTGGCACTATCTTGTACCAATCAA—TACACCATATTCAAAG	2226
Sbjct	2168	CCACTACCCATACAGGCTTGGCACTACCCCTGCACTGCAACTTT—ACCATTTCAAGG	2226
Query	2227	TCAGGATGTACGTGGGGAGG—GTGAGCACAGGCTGGAAAGCGGGCTGCAACTGGACGGG	2285
Sbjct	2227	TTAGGATGTACGTGGG—GGGAGTGGAGCACAGGCTGGAAAGCCATCAATTGGACTCGA	2285
Query	2286	GGCGAACGCGTGTGATCTGGAAAGACAGGGACAGGCTGGAGCTCAGCCGTTGCTGTCC	2345
Sbjct	2286	GGAGAGCGTGTGTAACCTGGAGGACAGGGACAGATCAGAGCTTACCCCGCTGCTGTCT	2345
Query	2346	ACACACAGTGGCAGGTCTT—CCGTGTTCTTCACGACCCCTGCCAGC—CTTGTCAACCG	2403
Sbjct	2346	ACAACGGAGTGGCAGGT—TTGCCCTGTTCTTCACCCCTACCGCTCT—GTCCACTG	2403
Query	2404	GCCTCATCCACCTTACAGACATGTGGACGTGGAGTACTGTACCGGGTACGGTCAA	2463
Sbjct	2404	GTTGATCCATCTTACAGAACGTGGAGCTACAAACCTGTACGGTATAAGGGTCG—	2462
Query	2464	GCA—TCT—CGTCCTGGGCCATTAAAGTGGGAGTACGTGCT—TCTCTGTTCTCTGCTTG	2520
Sbjct	2463	GGCGTTGTC—TCCTTGCATCAATGGGAGTATGTCCTG—TGCTTCTCTCTCTGG	2520
Query	2521	CAGACGGCGCGCTGCT—CCTGCTTGTGGATGATGTTACTCATATCCCAAGCGGGAGGG	2579
Sbjct	2521	CGGACGGCGCGCTGCT—TGCCCTGCTTGTGGATGATGCTGCTGATAGCTCAAGCTGAGGCC	2579
Query	2580	GCTTGGAGAACCTCGTAATCTCAATGCAAGCATCCGCCGGGAGGCCAGGGTC—TTGT	2638
Sbjct	2580	GCCCTAGAGAACCTGGTGGCTCAACCGCGCATCCGTGGCCGGGGCATGG—CATTTCT	2638

Query	2639	GTCCTTCTCGTCTCTGCTT-TGGTGGTATC-TGAAGGGTAGG-TGGGTGCC-G	2694
Sbjct	2639	CTCCTTCTCGTCTCTGCTT-TGCTGCTGGA-CATCAAGGGCAGGCTGG-T-CCCTG	2694
Query	2695	GAGCGGTC-TACGCCCTACCGG-GATGTGGCTCTCCCTGCTCTGCTGGCGTTGCC	2752
Sbjct	2695	GGGGGG-CATATGCCCTACCGGC-TAIGGCCCTACTCTGCTCTGCTGGCGTTACC	2752
Query	2753	TC-AGCGGGCATACCGC-ACTGGACACGG-AGGTGGCCGCTGGTGGCGCGTTGTCT	2809
Sbjct	2753	ACCA-CGAGCATACCCA-TGGAC-CGGGAGATGGCAGCATCGTGGCGAGGCCGCGTT-T	2808
Query	2810	T-GTCGGGT-TAATGGCC-T-GACTCT-GTCGCCATTACAAAGC-GCTATATCAGCT-G	2863
Sbjct	2809	TGGTAGG-TCTGATA-CTCTTGAC-CTTGTACCGCACTATAAGCTGTCC-TC-GCTAG	2863
Query	2864	G-TGCAITGGTGGCTT-CAGTATTTCTGACCAGAGTAAAGCGCAACT-GCACGTGTG	2920
Sbjct	2864	GCT-CATATGGTGG-TTACAATATTTACCAAGGGCCAGGGCACA-CTTGCAGGTGTG	2920
Query	2921	GGTcccccccTCACGTCGggggggggCGCGATGCCGTCATCTTACTCATGTTGT-AG	2979
Sbjct	2921	GATCCCCCCCCCTAACGTCGGGGGGGGCGATGCCGTCATCTCCACGTCGGCGA-	2979
Query	2980	TACACCC-GACCCCTGGTATTGAC-ATCACAAACTACTC-CTGGCCAT-CTTCGGACCC	3035
Sbjct	2980	TCCACCCAGAGC-TAATCTT-ACCATCACCAAAAT-CTTGTCTGCCATACT-CGGTCCA	3035
Query	3036	CTT-TGGATTCCTAACGCCAGTTG-CTTAAAGTCCCTACTCTGCGGTTCAAGGCC	3093
Sbjct	3036	CTCATGG-TGTCACGGCTGGTAAAC-AAGTGGCGTACTCTGCGGCCACACGGGC	3093
Query	3094	TTC-TCCG-G-ATCTGCGCGTAGCGCGGAAGATAGCCGGAGGTATTACGTGCAAATGG	3150
Sbjct	3094	T-CATTCTGTGCAT--GCATGCTGGTGCAGGAAGGTCTGGGGTCATTATGCTCAAATGG	3150
Query	3151	C-CATCATCAAGTTAGGG-GCCCTTACTGGCACCTATGTTATAACCATCTCACCCCTCT	3208
Sbjct	3151	CTC-TCATGAAGTT-GGCCGCACTGACAGGTACGTCTTATGACCATCTCACCCCTCT	3208
Query	3209	TGGAGACTGGCGCACACGG-CCTGCGAGAICTGCCGCGTGGCTGTGGAAACCCAGTCGCT	3267
Sbjct	3209	GCGGGACTIONGGCCACAG-CGGGCTACGAGACCTTGGCGTGGCAGTTGAGCCCGTGTCT	3267
Query	3268	TCTCCGA-ATGGAGACCAAGCTCATCAGTGGGGGCCAGATACCGCCGGTGGCGTAC	3326
Sbjct	3268	TCTCT-GATAATGGAGACCAAGGTATCACCTGGGGGCCAGACACCGCCGGTGGGGAC	3326
Query	3327	ATCATCAACGGCTTCTGCCGTCTGCCGTAGGGGCCAGG-AGATAC-TGCTGGG-CCA	3383
Sbjct	3327	ATCATCTGGGCTCTGCCGTCTCCCCCCCAAGGGG-AGGGAGATACAT-CT-GGGACCG	3383
Query	3384	GCCGACGGAATGGTCTC-CAAGGGTGGAGGTGCTGGCGCCATCACGGCGTACGCCCA	3442
Sbjct	3384	GCAGACAGCCTGAGGCCA-GGGGIGGGACTCTCGCCCTATTACGGCTACTCCCA	3442
Query	3443	GCGACAGGAGGCCCTCTAGGGTGTATAATCACCGCCTGACTGCGGGACAAAACCA	3502
Sbjct	3443	ACAGACGCGAGGCCCTACTTGGCTGCATCATCACTAGCCTCACAGGCCGGACAGGAACCA	3502
Query	3503	AGTGGAGGGTGAAGTCCA-GATCGTCAACTGCTACCCAAACCTTCTGGCAACGTGCA	3561
Sbjct	3503	GGTCGAGGGGGAGGTCAGAAGTGGCTCACCACCGCAACACAATCTTCTGGCGACCTCGG	3561
Query	3562	TCAATGGGTATGCTGGACTGTCTACACCGGGGCCAGCAGGACCATCGCATACCCA	3621
Sbjct	3562	TCAATGGCTGTGGACTGTCTATCATGGTGGCGCTAAAGACCCCTTGGCG-CCCA	3620
Query	3622	A-GGGTCTGTCTACAGATGTATAACCAATGTGGACCAAGACCTTGTGGCTGGCCCGT	3680
Sbjct	3621	AAGGGCCAAATACCCAAATGTACACCAATGTGGACCAAGGACCTCGTGGCTGGCAAGCG	3680
Query	3681	CCTCAAGGTTCCCGTCACTGACACCCCTGACTCTGGCGCTCTGGACCTTACCTGTC	3740
Sbjct	3681	CCCCCGGGGGCGCTTCTGACACCATGCACTGGCGAGCTGGACCTTACTTGGTC	3740

Query	3741	ACGAGGCACGCCGATGTCATTCCCGTGCGCCGGCGAGGTGATAGCAGGGGTAGCCTGCTT	3800
Sbjct	3741	ACGAGGCATGCCGATGTCATTCCCGTGCGCCGGCGAGGTGATAGCAGGGGTAGCCTGCTT	3800
Query	3801	TCGCCCC-GGCCATTCTACTTGAAGGCTCCCTCGGGGGTCCGCTGTTGTGCCCGC	3859
Sbjct	3801	TC-CCCCAAGGCCGCTCTACTTGAAGGCTCTCCGGCGTCACTGCTCTGCCCTC	3859
Query	3860	GGGACACGCCGTGGCCATT-CAGGGCCGCGGTGTCACCCGTGGAGTGGCTAAAGCGG	3918
Sbjct	3860	GGGGCACGCGTGGCATTTC-GGGCTGCGTGTGACCCGAGGGTTGCGAAGGGCG	3918
Query	3919	TGGACTTTAT-CCCTGTGGAGAACCTAGGGACACCA-T--GAGATCCCCGGTGTACAG	3974
Sbjct	3919	TGGACTTTGTACCC-GTCGAGT-C-TATGGA-AACCACTATGCGTCCCCGGTCTTCACG	3974
Query	3975	GACAACCTCTCACCAGCAGTGGCCAGAGC-TTCCAGGTGGCCACCTGCATGCTCC	4033
Sbjct	3975	GACAACCTCGTCCCCCTCCGGCGTACCGCAGA-CATTCAAGGTGGCCATCAGCG-CC	4032
Query	4034	C-ACCGGCAGCGGTAAAGAGCACCAAGGTCCCGCTGCGTACGCAGCCCA-GGGCTACAAAG	4091
Sbjct	4033	CTACTGGTAGGGCAAGAGCACTAACAGTGGCGCTGGTATGAGCCAAAGGG-TATAAG	4091
Query	4092	GTG-TTGGTGCTCAACCCCTCTGTTGTCACCGCTGGGCTT-GGTGCTTACATGTC	4149
Sbjct	4092	GTGTTG-TCTCTGAAACCGTCCGTCGCCACCTAGG-TTTCGGGGCTATATGCTA	4149
Query	4150	AGGCCATGGGGTGTATCTAATATCAGGACCGGGTGGAGAACAAATTACACTGGCAGCC	4209
Sbjct	4150	AGGCCATGGTATGCCCTAACATCAGAACCGGGTAAAGGACCATCACACGGT-GCC	4208
Query	4210	CC-ATCACGTACTCCACCTACGGCAAGTCTTGCACGGCGGGTGCCTAGGAGGTGCT	4268
Sbjct	4209	CCCATCACGTACTCCACCTATGGCAAGTTCTTGCACGGTGGTGCCTCTGGGGGCC	4268
Query	4269	TATGACATAATAATTGTGACGAGTGCACCTCCACCGA-T-G-CACACATCCATTGGC	4325
Sbjct	4269	TATGACATCATATAATGATGAGTGCACACTCAACTGACTCGACAC-T-ATCTGGC	4325
Query	4326	ATCGGCACTGCTCTGACCAAGCAGAGACTGCGGGGGCAGACTGGTTGTGCTGCCACT	4385
Sbjct	4326	ATCGGCACAGTCTGGACCAAGCGAGACGGCTGGACCGGACTCGTGTCTGCCACC	4385
Query	4386	GCTACCCCTCGGGCTCGTCACTGTGTCC-CATCTAACATCGAGGAGGGTTGCTCTGTC	4444
Sbjct	4386	GCTACGCCCTCGGGATCGGTACCCGT-CCACATCAAACATCGAGGAGGGTGGCTCTGTC	4444
Query	4445	CACCAACGGAGAGATCCCCTTAACGGCAAGGCTATCCCCCTCGAGGTGATCAAGGGGG	4504
Sbjct	4445	CACCACTGGAGAAATCCCCTTATGGCAAGGCAACATCCCCATCGAGGACATCAAGGGGG	4504
Query	4505	AAGACATCTCATCTTGCACCTCAAAGAAGAAGTGCACGAGCTCCCGCGAAGCTGGT	4564
Sbjct	4505	GAGGCACCTCATTTTCTGCCATTCAGAACAGAACATGATGAGCTCCCGCGAAGCTG-T	4563
Query	4565	C-G-CATTGGGCATCAATGGCGTGGCTACTACCGCGCTTGTGACTGCTGTCATCCCG	4622
Sbjct	4564	CCGGCCTCGGAC-TCAATGCTGTAGCATATTACGGGGCTTGTGATCGTCAATCCA	4622
Query	4623	ACACGGCGGATGTGCGTGTGACCGAGTCTCATGACTGGCTTACCGGGGA	4681
Sbjct	4623	ACTACGGCGGAGACGTCAATGTCGTAG-CAACGGGACGCTCAATGACGGGGCTTACCGGGGA	4681
Query	4682	CTTCGACTCTGTGATAGACTGCAACACGGTGTCACTCGACAGCTGATTCAGCCTG	4741
Sbjct	4682	TTTCGACTCTGTGACTGCAACATGATGTCACCCAGACAGCTGACTTCAGCCTGGA	4741
Query	4742	CCCTACCTTACCATGAGAACACAC-GCTCCCCAGGATGCTGCTCCAGGACTCA-A	4799
Sbjct	4742	CCCGACCTTCACCATGAGACGACGCCG-TGCCACAAGACGCCGTC-ACG-CTCGCA	4798
Query	4800	-CGCGGGGGAGGACTGGCAGGGG	4822
Sbjct	4799	CGCGCGAGGAGCAGTGGTAGGGG	4822

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